Specific or generic? Using bioinformatics and ocean metagenomic databases to select primers that best reflect plankton community composition.

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Harmful algal blooms are a major concern for coastal communities around the world, specifically *Pseudo-nitzschia* blooms that can produce domoic acid that bioaccumulates within filter-feeding shellfish. HABs can force fishery and aquaculture closures to prevent outbreaks of amnesic shellfish poisoning among consumers, as in 2016 and 2017 when Narragansett Bay fisheries were closed due to high levels of domoic acid detected in shellfish. The RI-CAIM Narragansett Bay Observatory is composed of two biogeochemical sensor buoys, one in the north of Greenwich Bay and the other off the western coast of Jamestown (co-located with the URI GSO Long Term Plankton Times Series). These systems are collecting real-time biogeochemical and meteorological data. In order to predict HAB formation,we are working to develop a computer model capable of predicting future blooms using Observatory data. To validate the prediction model we will deploy a remote phytoplankton sampling system on one of the buoys that will collect plankton samples during predicted bloom periods that will be processed for metagenomic barcoding and metatranscriptome analysis in order to determine community composition and transcription profiles. In order to amplify the ribosomal SSU DNA of phytoplankton and associated bacteria, PCR primers targeting them are necessary. This project will evaluate a bioinformatic pipeline that will compare eukaryotic specific 18S as well as 16S bacterial specific SSU primers currently used to a single universal primer that can capture both to determine which primers have the best sensitivity and specificity for phytoplankton using metagenomic data from several ocean databases. Accurate community composition and relative frequencies within the plankton community will help to shed light on what triggers a *Pseudo-nitzschia* bloom and production of domoic acid.